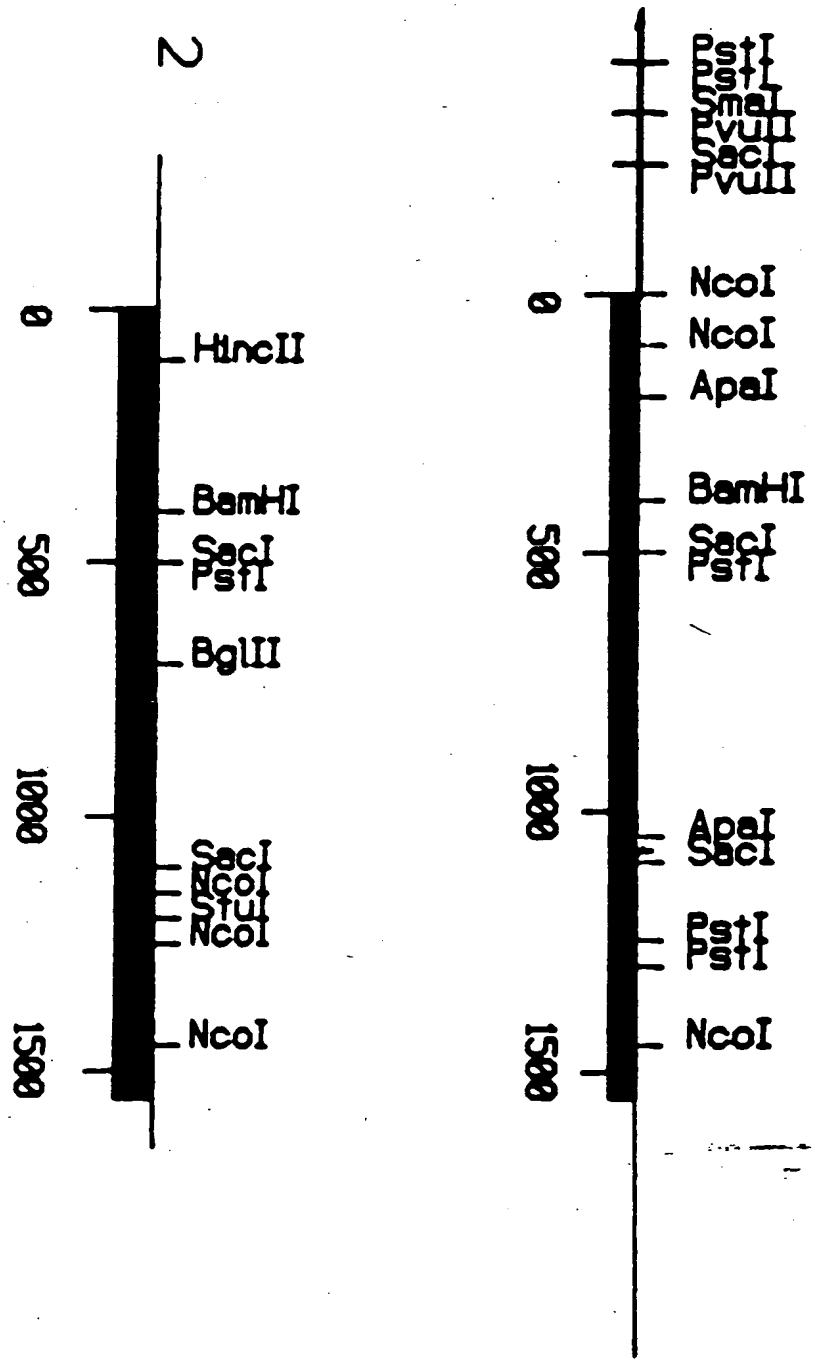
rat alpha 2
0
500
1000
1500
HincII
BamHI
SacI
PstI
BglII
SacI
NcoI
StuI
NcoI
NcoI
H alpha 2
(2600 bp)
0
500
1000
1500
PstI
PstI
SmaI
PvuII
SacI
PvuII
NcoI
NcoI
ApaI
BamHI
SacI
PstI
ApaI
SacI
PstI
PstI
NcoI

FIGURE 1

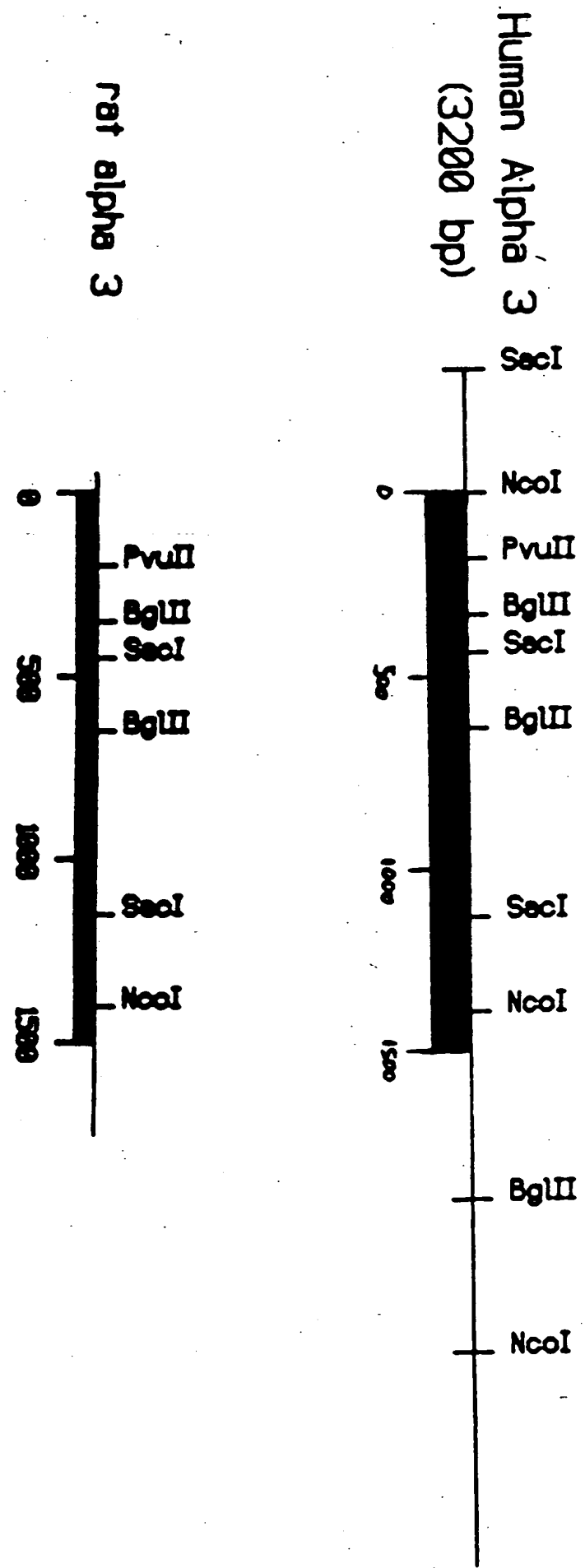
Human Alpha 3
(3200 bp)
SacI
NcoI
PvuII
BglII
SacI
BglII
SacI
NcoI
BglII
NcoI
rat alpha 3
PvuII
BglII
SacI
BglII
SacI
NcoI

FIGURE 2

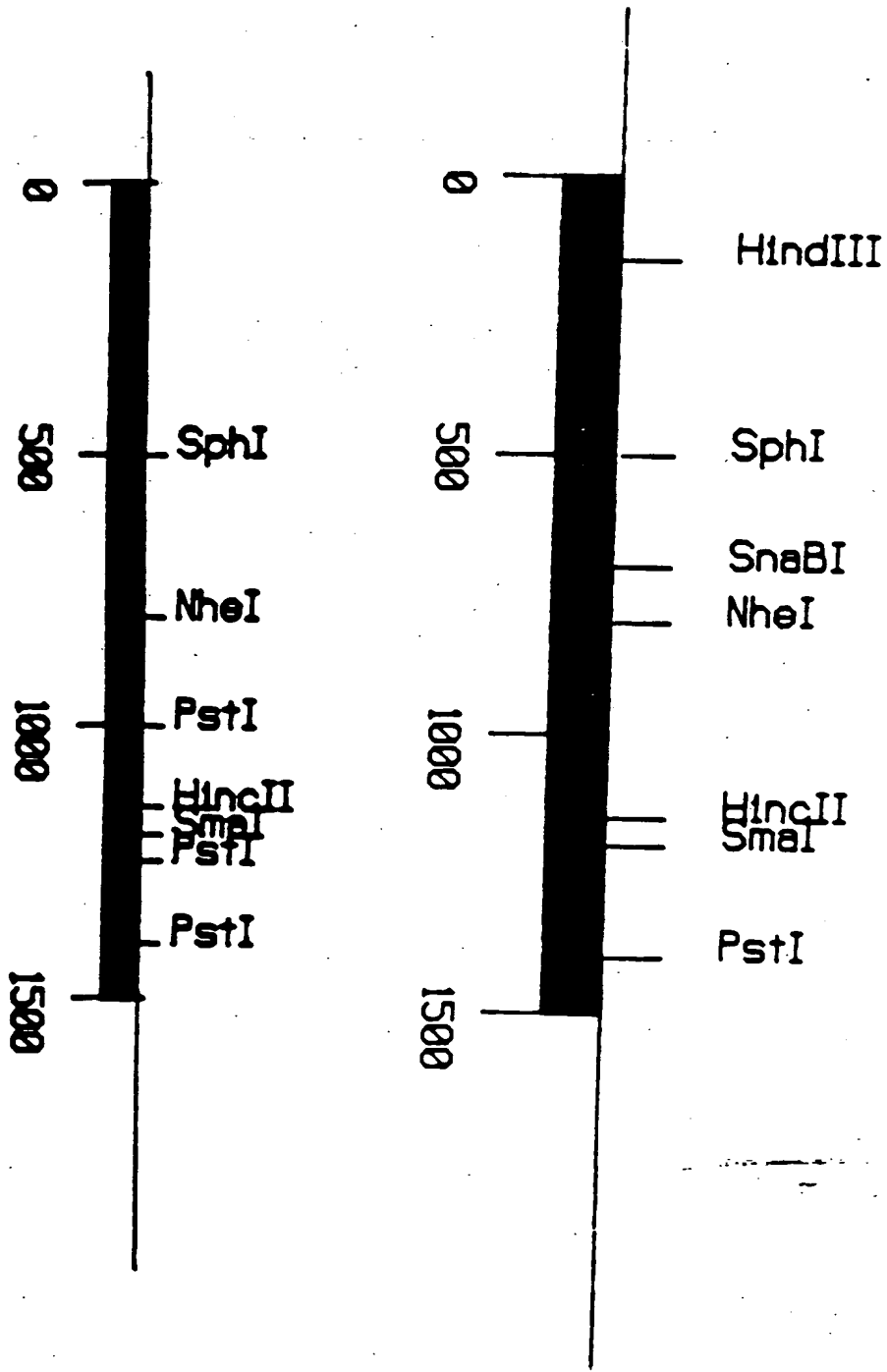
rat beta 2
0
500
1000
1500
SphI
NheI
PstI
HincII
SmaI
PstI
PstI
H Beta 2
(2450 bp)
0
500
1000
1500
HindIII
SphI
SnaBI
NheI
HincII
SmaI
PstI

FIGURE 3

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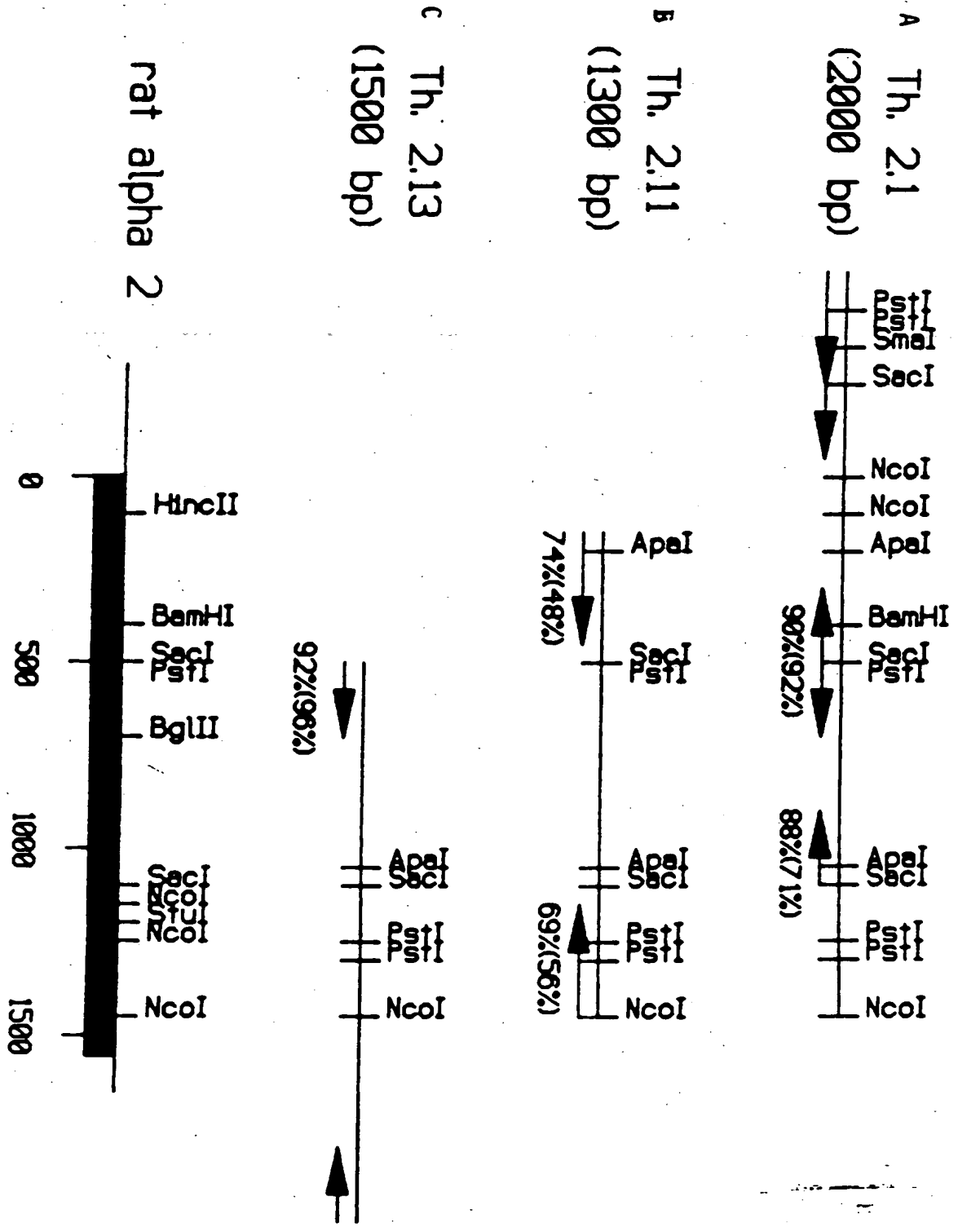

FIGURE 1

FIGURE 5

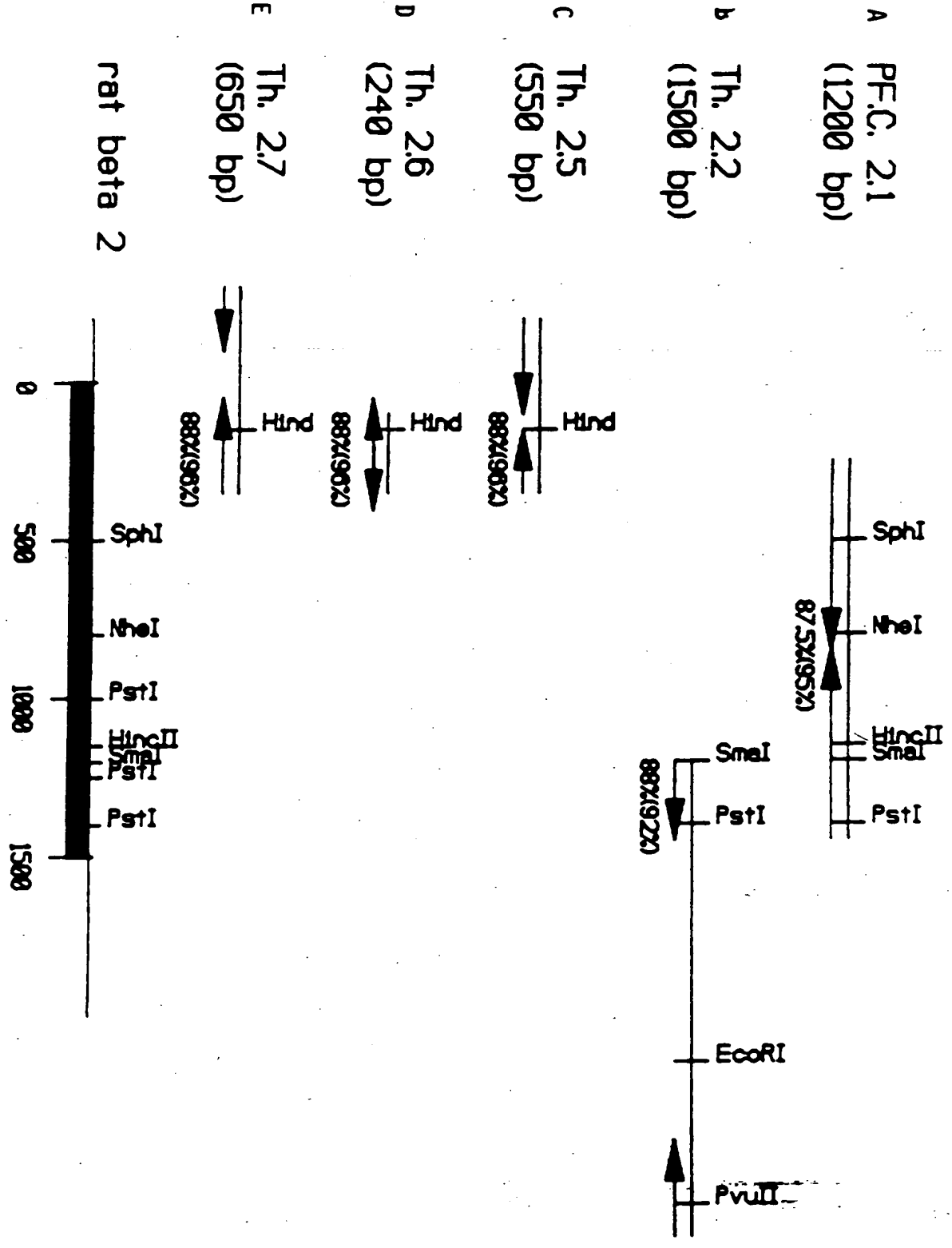
A PF.C. 2.1 (1200 bp)
B Th. 2.2 (1500 bp)
C Th. 2.5 (550 bp)
D Th. 2.6 (240 bp)
E Th. 2.7 (650 bp)
rat beta 2
0
500
1000
1500
SphI
NheI
PstI
HincII
SmaI
PstI
PstI
SmaI
PstI
EcoRI
PvuII
HindIII
HindIII
HindIII

FIGURE 6

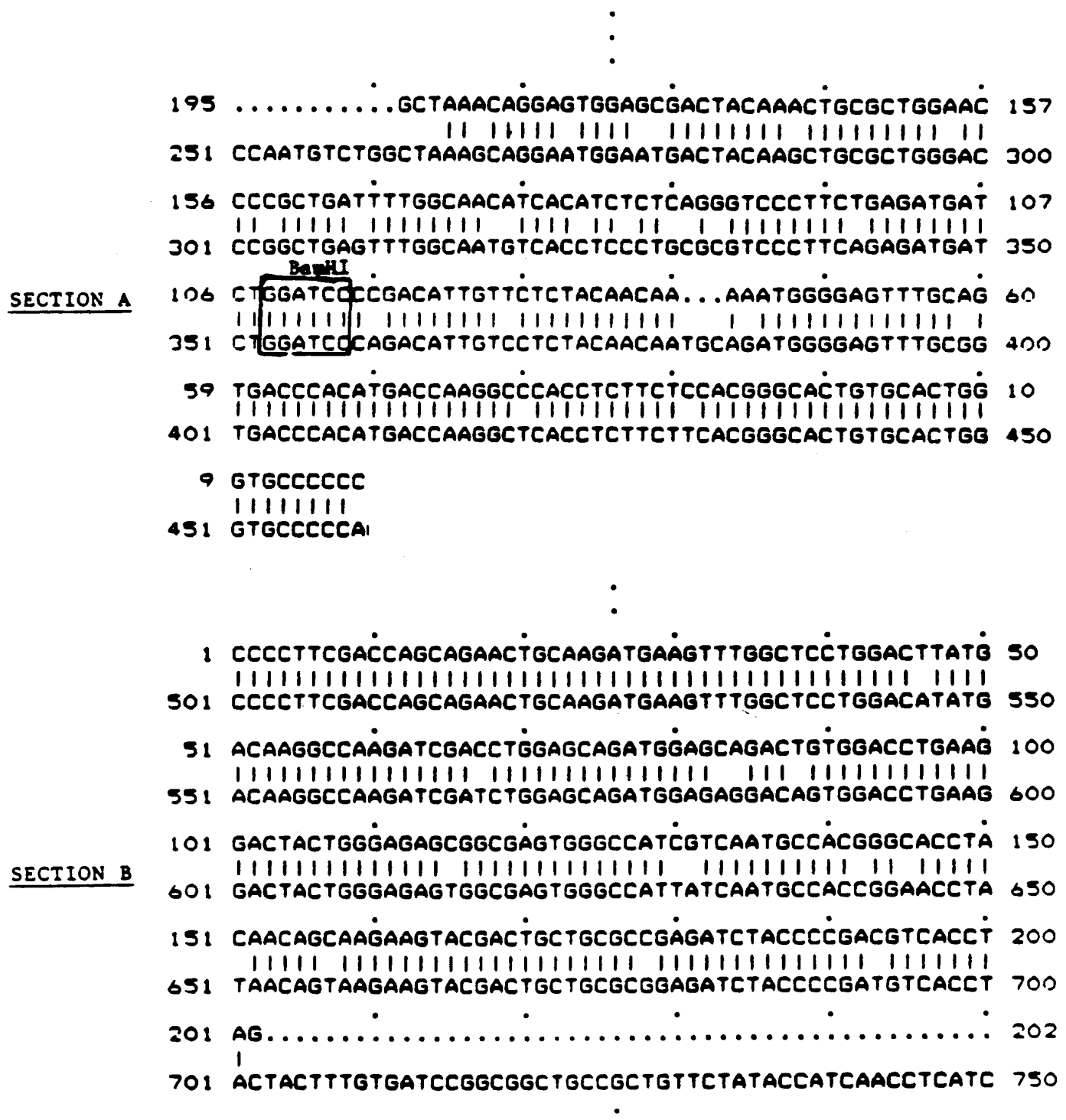
SECTION A
SECTION B
BamHI
195 .....GCTAAACAGGAGTGGAGCGACTACAAACTGCGCTGGAAC 157
251 CCAATGTCTGGCTAAAGCAGGAATGGAATGACTACAAGCTGCGCTGGGAC 300
156 CCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGAT 107
301 CCGGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT 350
106 CTGGATCCCCGACATTGTTCTCTACAACAA...AAATGGGGAGTTTGCAG 60
351 CTGGATCCCAGACATTGTCCTCTACAACAATGCAGATGGGGAGTTTGCGG 400
59 TGACCCACATGACCAAGGCCCACCTCTTCTCCACGGGCACTGTGCACTGG 10
401 TGACCCACATGACCAAGGCTCACCTCTTCTTCACGGGCACTGTGCACTGG 450
9 GTGCCCCCC
451 GTGCCCCCA
1 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACTTATG 50
501 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACATATG 550
51 ACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAG 100
551 ACAAGGCCAAGATCGATCTGGAGCAGATGGAGAGGACAGTGGACCTGAAG 600
101 GACTACTGGGAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTA 150
601 GACTACTGGGAGAGTGGCGAGTGGGCCATTATCAATGCCACCGGAACCTA 650
151 CAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTACCCCGACGTCACCT 200
651 TAACAGTAAGAAGTACGACTGCTGCGCGGAGATCTACCCCGATGTCACCT 700
201 AG..... 202
701 ACTACTTTGTGATCCGGCGGCTGCCGCTGTTCTATACCATCAACCTCATC 750

FIGURE 7

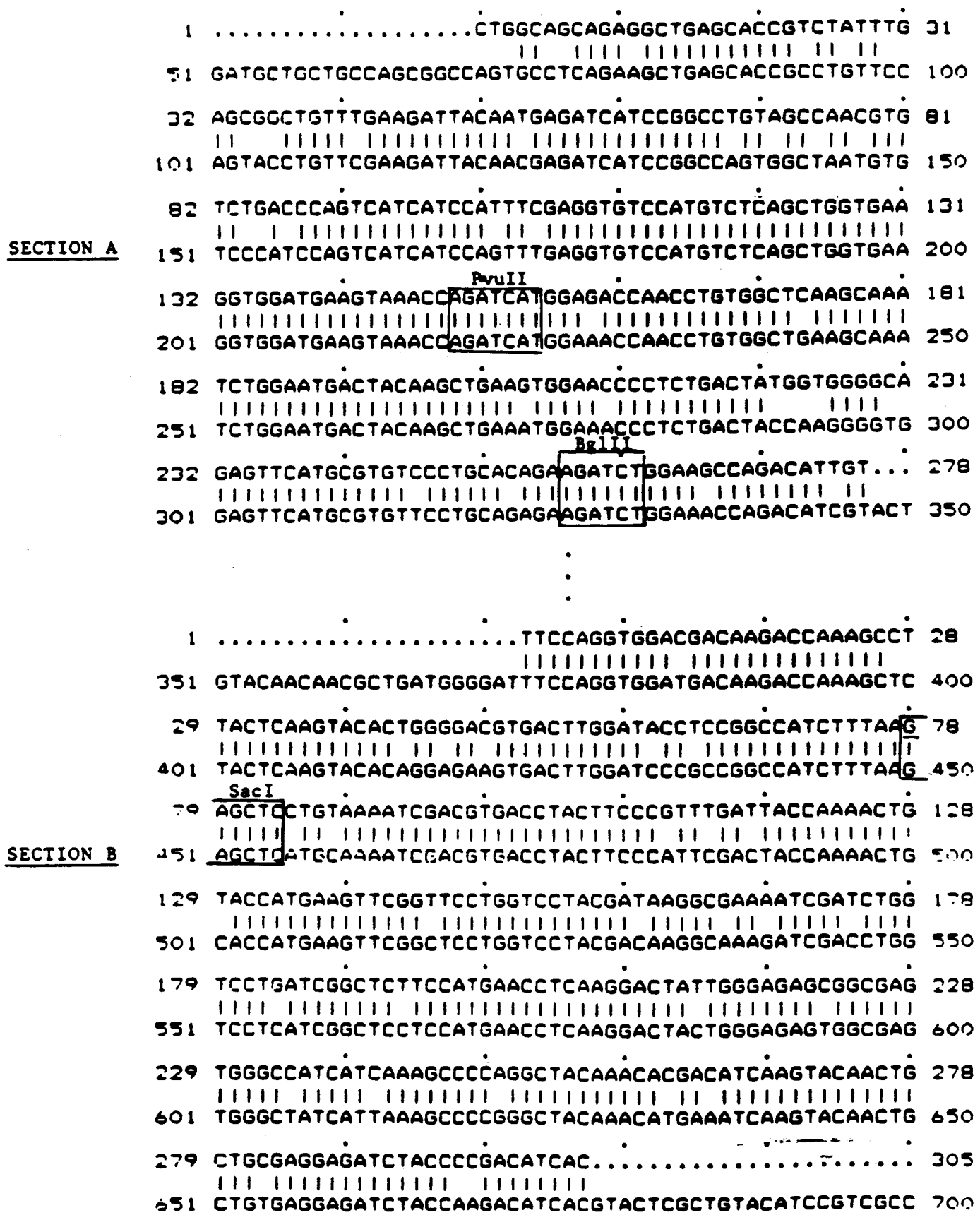

FIGURE 8

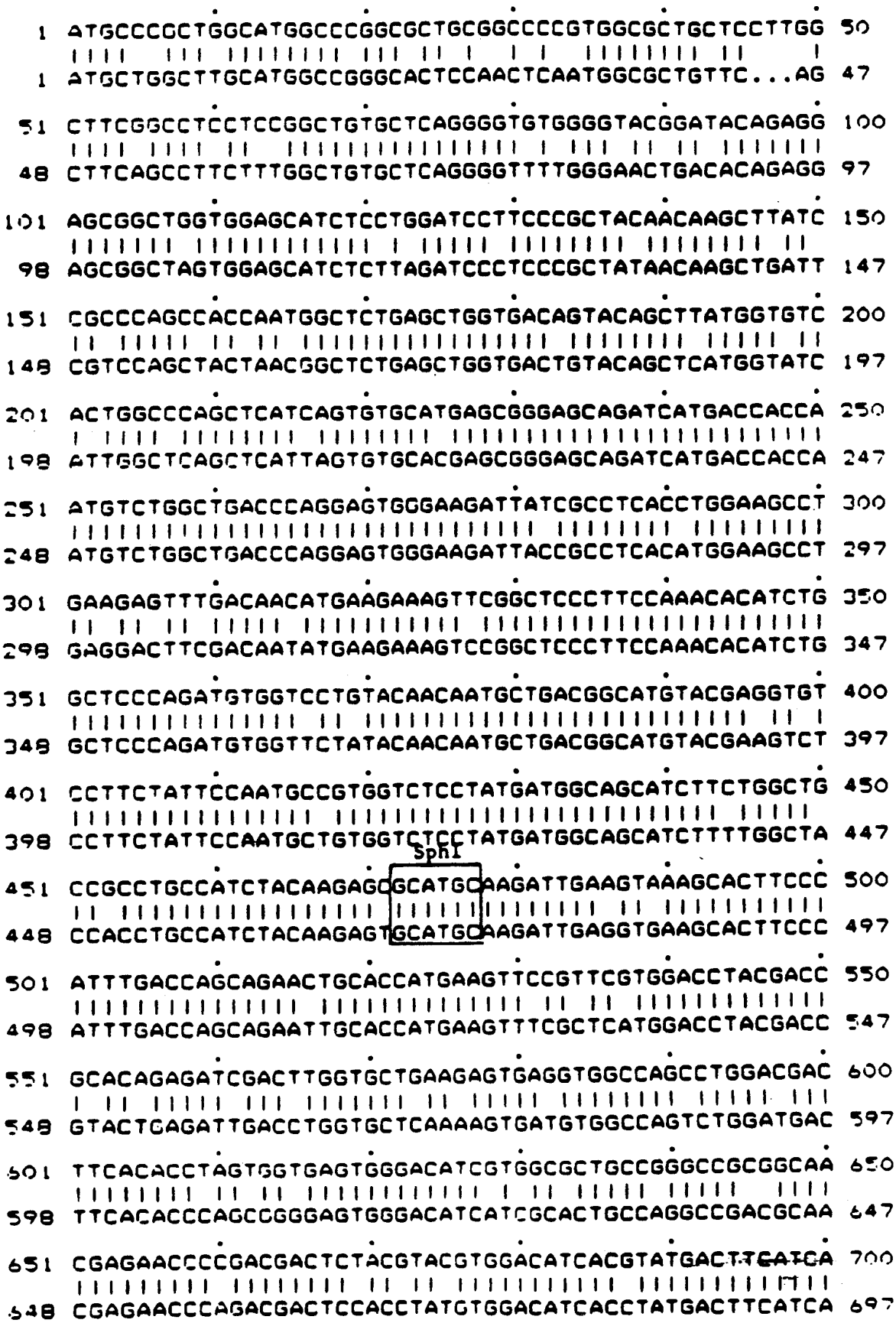

FIGURE 9(a)

```
701 TTCGCCGCAAGCCGCTCTTCTACACCATCAACCTCATCATCCCCTGTGTG 750
    |||| ||||| || |||||||||| ||||||||||||||||||| ||
698 TTCGTCGCAAACCACTCTTCTACACTATCAACCTCATCATCCCCTGCGTA 747

751 CTCATCACCTCGCTAGCCATCCTTGTCTTCTACCTGCCATCCGACTGTGG 800
    |||||||||||||| |||||||| |||||||||||| || ||||||||
748 CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG 797

801 CGAGAAGATGACGTTGTGCATCTCAGTGCTGCTGGCGCTCACGGTCTTCC 850
     || |||||||| | || || || |||||||| || |||||||| ||||
798 TGAAAAGATGACACTTTGTATTTCTGTGCTGCTAGCACTCACGGTGTTCC 847

851 TGCTGCTCATCTCCAAGATCGTGCCTCCCACCTCCCTCGACGTGCCGCTC 900
    |||||||||||||||||| |||||||||||||||||| || |||||
848 TGCTGCTCATCTCCAAGATTGTGCCTCCCACCTCCCTCGATGTACCGCTG 897

901 GTCGGCAAGTACCTCATGTTCACCATGGTGCTTGTCACCTTCTCCATCGT 950
    || |||||||||||||||| |||||||||| ||||||||||||||||
898 GTGGGCAAGTACCTCATGTTTACCATGGTGCTAGTCACCTTCTCCATCGT 947

951 CACCAGCGTGTGCGTGCTCAACGTGCACCACCGCTCGCCCACCACGCACA 1000
    |||||||||||| |||||||| |||||||||||||||| ||||||||||
948 CACCAGCGTGTGTGTGCTCAATGTGCACCACCGCTCGCCTACCACGCACA 997

1001 CCATGGCCCCCTGGGTGAAGGTCGTCTTCCTGGAGAAGCTGCCCGCGCTG 1050
     ||||||| |||||||| ||||| ||||||||||||||||||| | |||
998 CCATGCCCCCCTGCGTCAAGGTGGTCTTCCTGCAGAAGCTGCCCACCCTG 1047

1051 CTCTTCATGCAGCAGCCACGCCATCATTGCGCCCGTCAGCGCCTGCGCCT 1100
     |||||| |||||||||||||||| | || || |||||||| |||||| |
1048 CTCTTCCTGCAGCAGCCACGCCACCGCTGTGCACGTCAGCGTCTGCGCTT 1097

1101 GCGGCGACGCCAGCGTGAGCGCGAGGGCGCTGGAGCCCTCTTCTTCCGCG 1150
     | || | |||||||| ||||| |||||| | || | |||||||| |
1099 GAGGAGGCGCCAGCGAGAGCGTGAGGGC...GAGGCGGTTTTCTTCCGTG 1144

1151 AAGCCCCAGGGGCCGACTCCTGCACGTGCTTCGTCAACCGCGCGTCGGTG 1200
     ||| || | ||| ||| | || || ||||| ||||||| || || |||
1145 AAGGTCCTGCGGCTGACCCATGTACCTGCTTTGTCAACCCTGCATCAGTG 1194

1201 CAGGGGTTGGCCGGGGCCTTCGGGGCTGAGCCTGCACCAGTGGCGGGCCC 1250
     ||||| ||||| ||||| ||| | |||||||| | || || |||||
1195 CAGGGCTTGGCTGGGGCTTTCCGAGCTGAGCCCACTGCA...GCCGGCCC 1241

1251 CGGGCGCTCAGGGGAGCCGTGTGGCTGTGGCCTCCGGGAGGCGGTGGACG 1300
      |||||||| | || ||| || |||||||||||||||| || ||||| |
1242 GGGGCGCTCTGTGGGGCCATGCAGCTGTGGCCTCCGGGAAGCAGTGGATG 1291

1301 GCGTGCGCTTCATCGCAGACCACATGCGGAGCGAGGACGATGACCAGAGC 1350
     |||| |||||||| || |||||||||| || ||||| ||||||||||
1292 GCGTACGCTTCATTGCGGACCACATGCGAAGTGAGGATGATGACCAGAGT 1341

1351 GTGAGTGAGGACTGGAAGTACGTCGCCATGGTGATCGACCGCCTCTTCCT 1400
     ||||| |||||||||| ||||| |||||||||||||||||| ||||
1342 GTGAGGGAGGACTGGAAATACGTTGCCATGGTGATCGACCGCCTGTTCCT 1391
```

FIGURE 9(b)

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PstI

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1401 CTGGATCTTTGTCTTTGTCTGTGTCTTTGGCACCATCGGCATGTTCCTGC 1450
     ||||||||||||||||||||||||||||| ||| |||||||||||||||
1392 GTGGATCTTTGTCTTTGTCTGTGTCTTTGGGACCGTCGGCATGTTCCTGC 1441

1451 AGCCTCTCTTCCAGAACTACACCACCACCACCTTCCTCCACTCAGACCAC 1500
     ||||||||||||||||||||||  |||| |||||||||||| | ||||||
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTTCCTCCACCCTGACCAC 1491

1501 TCAGCCCCCAGCTCCAAGTGA 1521
     ||||| ||||||||||||||||
1492 TCAGCTCCCAGCTCCAAGTGA 1512
```

FIGURE 9(c)